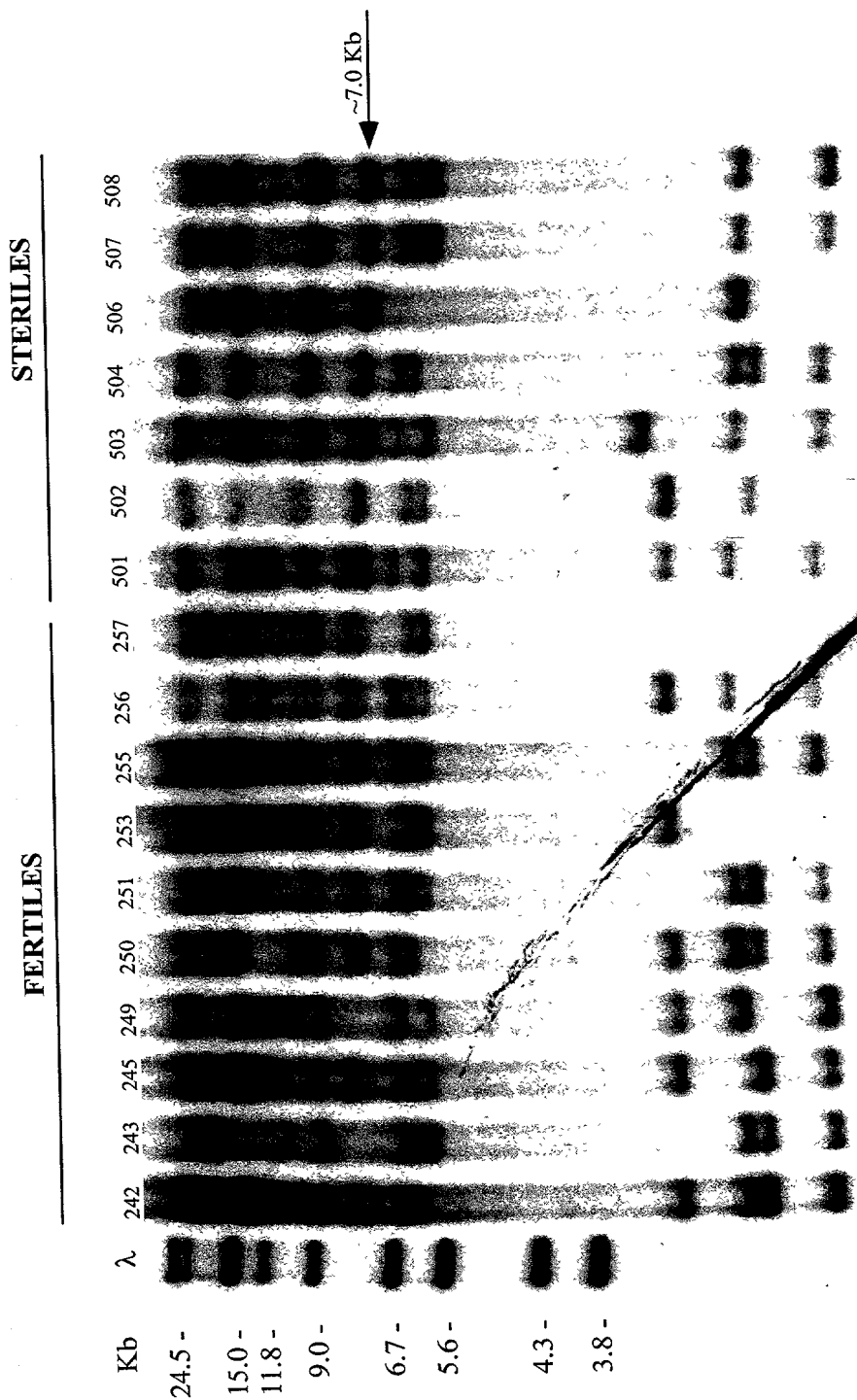


FIGURE 1



SOUTHERN OF ECORI DIGESTED DNA FROM THE MALE STERILE FAMILY BS92-7. HYBRIDIZED WITH THE MU1 TRANSPOSON.

Figure 2

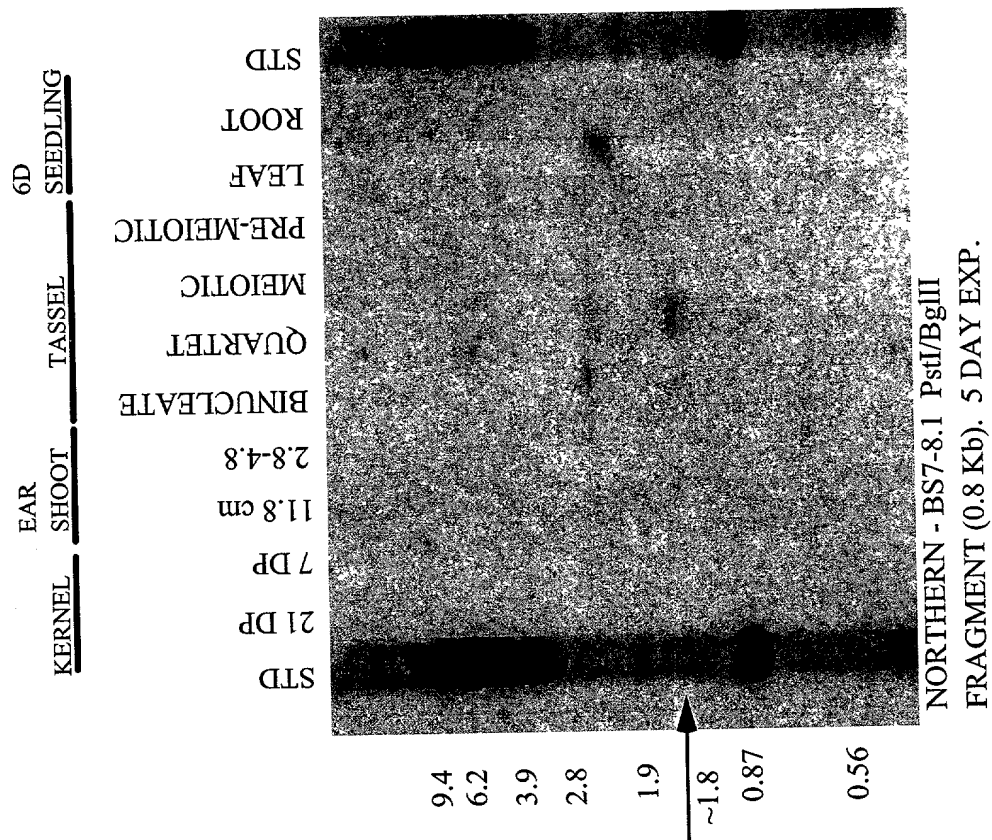


FIGURE 3

FIGURE 4

GGTGACCTCAAGCAAGGGCAAGGTATGCGTAACCGGGGCCTCAGGCTTTGTTGCCTCTTG  
1 -----+-----+-----+-----+-----+-----+-----+ 60  
CCACTGGAGTTCGTTCCCGTTCCATACGCATTGGCCCCGGAGTCCGAAACAACGGAGAAC

b        V T S S K G K V C V T G A S G F V A S W -

XhoI  
|

GCTTATCAAACGGCTCCTCGAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCCAGG  
61 -----+-----+-----+-----+-----+-----+ 120  
CGAATAGTTTGGCGAGGAGCTCAGACCTATAGTACACCATCCCTGACAGTCCCTGGGTCC

b        L I K R L L E S G Y H V V G T V R D P G -

AAATCACCAAAAAACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT  
121 -----+-----+-----+-----+-----+-----+ 180  
TTTAGTGGTTTTTTTGTGGGTGGAACCTTTAATGGACCGGATTCTCTCCGACGTTTA

b        N H Q K T A H L W K L P G A K E R L Q I -

CGTGCGAGCTAATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGGCCTGTGAGGG  
181 -----+-----+-----+-----+-----+-----+ 240  
GCACGCTCGATTAGACAACCTTCTTCCCTCGAAGCTGTCGCGGCACTACCGGACACTCCC

b        V R A N L L E E G S F D S A V M A C E G -

TGTATTCCACACTGCATCCCCGTCCTCGCTAAACCCGACTCTACTAGCAAGGAGGACAC  
241 -----+-----+-----+-----+-----+-----+ 300  
ACATAAGGTGTGACGTAGGGGGCAGGAGCGATTGTTGGGCTGAGATGATCGTTCCTCCTGTG

b        V F H T A S P V L A K P D S T S K E D T -

GCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGATCGTGCAAGAAGAACCCTT  
301 -----+-----+-----+-----+-----+-----+ 360  
CGAGCAGGGACGCCACTTGCCATGAGACTTGACGACTCTAGCACGTTCTTCTTGGGGAA

b        L V P A V N G T L N V L R S C K K N P F -

CCTGAAAAGGGTCGTCCTTACGTCTTCGTGCTGCGGTGAGGATCAGGGACGACGGTGG  
361 -----+-----+-----+-----+-----+-----+ 420  
GGACTTTTCCAGCAGGAATGCAGAAGCAGCAGACGCCACTCCTAGTCCCTGCTGCCACC

b        L K R V V L T S S S S A V R I R D D G G -

CCAGTCCAGTAACATCTCGCTGGACGAAACGACATGGAGCTCCGTGCCACTCTGCGAGAA  
421 -----+-----+-----+-----+-----+-----+ 480  
GGTCAGGTCATTGTAGAGCGACCTGCTTGTGTACCTCGAGGCACGGTGAGACGCTCTT

b        Q S S N I S L D E T T W S S V P L C E K -

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FIGURE 4B

GATGCATCTATGGTATGCCCTAGCCAAGGTATTTGCAGAGAAAGCGGCGTGGGAGTTTCGC  
 481 -----+-----+-----+-----+-----+-----+ 540  
 CTACGTAGATAACCATACGGGATCGGTTCCATAAACGTCTCTTTGCGCCGACCCTCAAGCG  
 b M H L W Y A L A K V F A E K A A W E F A -  
 CAAGGAGAACGGCATCGACCTTGTGACTGTCCTCCCGTCGTTTCGTGATCGGGCCAGTTT  
 541 -----+-----+-----+-----+-----+-----+ 600  
 GTTCCTCTTGCCGTAGCTGGAACACTGACAGGAGGGCAGCAAGCACTAGCCCCGGGTCAAA  
 b K E N G I D L V T V L P S F V I G P S L -  
 GTCCACGAGCTATGCGTTACCGCTTCAGACGTCCTAGGCCTATTCCAAGGCGACACGGC  
 601 -----+-----+-----+-----+-----+-----+ 660  
 CAGGGTGCTCGATACGCAATGGCGAAGTCTGCAGGATCCGGATAAGGTTCCGCTGTGCCG  
 b S H E L C V T A S D V L G L F Q G D T A -  
 AAGGTTTCAGCTCGTACGGAAGAATGGGGTACGTCCACATCGACGACGTTGCGAGCAGCCA  
 661 -----+-----+-----+-----+-----+-----+ 720  
 TTCCAAGTCGAGCATGCCTTCTTACCCCATGCAGGTGTAGCTGCTGCAACGCTCGTCGGT  
 b R F S S Y G R M G Y V H I D D V A S S H -  
 CATCCTGGTGTACGAGGTCCCCCAGGCCGCGGGAGGTACCTGTGCAGCTCAGTGGTGCT  
 721 -----+-----+-----+-----+-----+-----+ 780  
 GTAGGACCACATGCTCCAGGGGTCCGGCGGCCCTCCATGGACACGTCGAGTCACCACGA  
 b I L V Y E V P Q A A G R Y L C S S V V L -  
 GGACAACGACGAGCTGGTCTCCTCGCTCGCGAAACGCTACCCGATATTCCCCATACCCCG  
 781 -----+-----+-----+-----+-----+-----+ 840  
 CCTGTTGCTGCTCGACCAGAGGAGCGAGCGCTTTGCGATGGGCTATAAGGGGTATGGGGC  
 b D N D E L V S S L A K R Y P I F P I P R -  
 GAGGCTGAACAGCCCCTACGGCAAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGG  
 841 -----+-----+-----+-----+-----+-----+ 900  
 CTCCGACTTGTCGGGGATGCCGTTTCGTACGATGGTTCGACTTGTGCAGCTTCGACGTCCC  
 b R L N S P Y G K Q S Y Q L N T S K L Q G -  
 GCTGGGCTTCAAGTTTCAGAGGGGTGCAGGAGATGTTTCGACGACTGCGTGCAGTCGCTCAA  
 901 -----+-----+-----+-----+-----+-----+ 960  
 CGACCCGAAGTTCAAGTCTCCCCACGTCCTCTACAAGCTGCTGACGCACGTACGCGAGTT  
 b L G F K F R G V Q E M F D D C V Q S L K -  
 AGACCAGGGCCACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGGGGTGCCTCCTGTGAA  
 961 -----+-----+-----+-----+-----+-----+ 1020  
 TCTGGTCCCGGTGGACGACCTACGGGGGACACTTGACGCTACCCCCACGGAGGACACTT  
 b D Q G H L L E C P L \*

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FIGURE 4C

CGCCCGTTTTTTTTTTCTTCAATAATTCCACGTCATGTCACGGTGTCTCGCGCAGACT  
 1021 -----+-----+-----+-----+-----+-----+ 1080  
 GCGGGCAAAAAAAAAAAGAAGTTATTAAGGTGCAGTACAGTGCCACAGGAGCGCGTCTGA

GCTACTGTCAGGTGTCAGGGCGTCATAGCTCACGGGCTCTACGGCTACATGAATAAAATG  
 1081 -----+-----+-----+-----+-----+-----+ 1140  
 CGATGACAGTCCACAGTCCCGCAGTATCGAGTGCCCGAGATGCCGATGTACTTATTTTAC

TCACGCTAGCTCGTCATTTGCTTTGCCATTTAAAAAAAAAAAAAAAAAAAACTCGAG  
 1141 -----+-----+-----+-----+-----+-----+ 1197  
 AGTGCGATCGAGCAGTAAACGAAACGGTAAATTTTTTTTTTTTTTTTTTTTGGAGCTC

XhoI

|

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FIGURE 5

1 GAATTCTCGT CTCGGCGGTC AACTGAACCG TAAACAGTGG AAAGTGGATA  
51 CTCTTTCTCT CTCTGCAATC CGTGCCGTGG AAGCAAATGG CGCAGTCGCC  
101 TACTTATCAC ACCAACTTAT CACCTAGAAA AGCGACGCGT CCTGGATCGA  
151 TTGCAAATCT ACCTCCAACC AACCCAGCTT TGTATCTGCT TACTGTGATC  
201 ACCAAAGTTG TGCTGATACG ATGTGCGATT ATTGCTCTTT CTTCTCTAGA  
251 ATGTTCTCTG CGATGCTTTA TAAGAGAAGG TTGGTCAGCA TCGATCTCTG  
301 CCAGTGCTTA GCTGAGAACA TGGTGACCTC AAGCAAGGGC AAGGTATGCG  
351 TAACCGGGGC CTCAGGCTTT GTTGCCCTCT GGCTTATCAA ACGGCTCCTC  
401 GAGTCTGGAT ATCATGTGGT AGGGACTGTC AGGGACCCAG GTATTTGCGA  
451 AATATCATTA CTATCGTATC AGTCCTCTTT ATTACATTAA TAATTCTTGA  
501 TTACCAATTT TTTCTTTTTT TTTTTTGGTA ACCCACAAGG AAATCACCAA  
551 AAGACAGCCC ACCTTTGGAA ATTACCTGGC GCTAAAGAGA GGCTGCAAAT  
601 CGTGCGAGCT GATCTGTTGG AAGAAGGGAG CTTCGACAGC GCCGTGATGG  
651 CCTGTGAGGG TGTATTCCAC ACTGCATCCC CCGTCCTCGC TAAACCCGAC  
701 TCTACTAGCA AGGCATGCCA TCGCCGATA TATATATGCA TATCTGGACC  
751 ATGCATCCTA CTGCAGCCTT TTCTATACGG AAGCGCGTTG CATCTACCGT  
801 ACGTGAAGCT AGCTATCTAA GCTAAGCTGT TTTTCATGCA TGCATGGTGC  
851 AGGAGGACAC GCTCGTCCCT GCGGTGAACG GTACTCTGAA CGTGCTGAGA  
901 TCGTGCAAGA AGAACCCGTT CCTGAAAAGG GTCGTCTTA CGTCTTCGTC  
951 GTCTGCGGTG AGGATCAGGG ACGACGGTGG CCAGTCCAGT AACATCTCGC  
1001 TGGACGAAAC GACATGGAGC TCCGTGCCAC TCTGCGAGAA GATGCATGTG  
1051 AGATACTACT GAACAGTGTC TACTCTCTCT CTCTCTGTCA TCGATCTCAA  
1101 ACCGTGATCT GAAAAACACG CATGCGCGCA CACGTTGCCG TCGTCGTCCC  
1151 TTTTGTGTGT CACCCGAAGC TATGGTATGC CCTAGCCAAG GTATTTGCAG  
1201 AGAAAGCGGC GTGGGAGTTC GCCAAGGAGA ACGGCATCGA CCTTGTGACT  
1251 GTCTCCCGT CGTTCGTGAT CGGGCCCAGT TTGTCCCACG AACTATGCGT  
1301 TACCGCTTCA GACGTCCTAG GCCTATTCCA AGGTATTCAT CTCAATCATT

1005555-01280





Figure 6

```

301 CCAGTGTCTAGCTGAGAACATGGTGACCTCAAGCAAGGGCAAGGTATGCG 350
      |||||||||||||||||||||||||||||||||||||||
1  .....GGTGACCTCAAGCAAGGGCAAGGTATGCG 29

351 TAACCGGGGCCTCAGGCTTTGTTGCCTCTTGGCTTATCAAACGGCTCCTC 400
      |||||||||||||||||||||||||||||||||||||||
30 TAACCGGGGCCTCAGGCTTTGTTGCCTCTTGGCTTATCAAACGGCTCCTC 79

401 GAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCCAGGTATTTGCGA 450
      |||||||||||||||||||||||||||||||||||
80 GAGTCTGGATATCATGTGGTAGGGACTGTCAGGGACCC..... 117

      .
      .

501 TTACCAATTTTTCTTTTTTTTTTTTGGTAACCCACAAGGAAATCACCAA 550
      |||||||||||||||
118 .....AGGAAATCACCAA 130

551 AAGACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT 600
      || |||||||||||||||||||||||||||||||||||
131 AAAACAGCCACCTTTGGAAATTACCTGGCGCTAAAGAGAGGCTGCAAAT 180

601 CGTGCGAGCTGATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGG 650
      ||||||||| |||||||||||||||||||||||||||
181 CGTGCGAGCTAATCTGTTGGAAGAAGGGAGCTTCGACAGCGCCGTGATGG 230

651 CCTGTGAGGGTGTATTCCACACTGCATCCCCCGTCCTCGCTAAACCCGAC 700
      |||||||||||||||||||||||||||||||||||
231 CCTGTGAGGGTGTATTCCACACTGCATCCCCCGTCCTCGCTAAACCCGAC 280

701 TCTACTAGCAAGGCATGCCATCGCCGCATATATATATGCATATCTGGACC 750
      |||||||||
281 TCTACTAGCA..... 290

      .
      .

851 AGGAGGACACGCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGA 900
      |||||||||||||||||||||||||||||||||||
291 AGGAGGACACGCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGA 340

901 TCGTGCAAGAAGAACCCGTTCTGAAAAGGGTCGTCTTACGTCTTCGTC 950
      ||||||||||||| |||||||||||||||||||
341 TCGTGCAAGAAGAACCCCTTCTGAAAAGGGTCGTCTTACGTCTTCGTC 390

951 GTCTGCGGTGAGGATCAGGGACGACGGTGGCCAGTCCAGTAACATCTCGC 1000
      |||||||||||||||||||||||||||||||
391 GTCTGCGGTGAGGATCAGGGACGACGGTGGCCAGTCCAGTAACATCTCGC 440

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FIGURE 6C

```

1751 AAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGGGCTGGGCTTCAA 1800
      |||||||||||||||||||||||||||||||||||||||||||||||
863  AAGCAGTCGTACCAGCTGAACACGTCGAAGCTGCAGGGGCTGGGCTTCAA 912

1801 GTTCAGAGGGGTGCAGGAGATGTTTCGACgACTGCGTACAGTCGCTCAAAG 1850
      |||||||||||||||||||||||||||||||||||||||||||||||
913  GTTCAGAGGGGTGCAGGAGATGTTTCGACGACTGCGTGCAGTCGCTCAAAG 962

1851 ACCAGGGACACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGGGTGCCTC 1900
      ||||||| ||||||||||||||||||||||||||||||||||| |||
963  ACCAGGGCCACCTGCTGGAGTGCCCCCTGTGAACTGCGATGGG..GGTGC 1010

1901 CGCCTGTGAACGCGCCGGTTGGGTTGCGTCCCGAACCCGCTGTAAATTCG 1950
      || ||||||||||||| |
1011 CTCCTGTGAACGCCC.....GTT 1028

1951 TTTTTTTTTTCTTCAATAATTCCACGTCATGTCACGGTGTCTCGCGCagA 2000
      |||||||||||||||||||||||||||||||||||||||||||||||
1029 TTTTTTTTTTCTTCAATAATTCCACGTCATGTCACGGTGTCTCGCGCAGA 1078

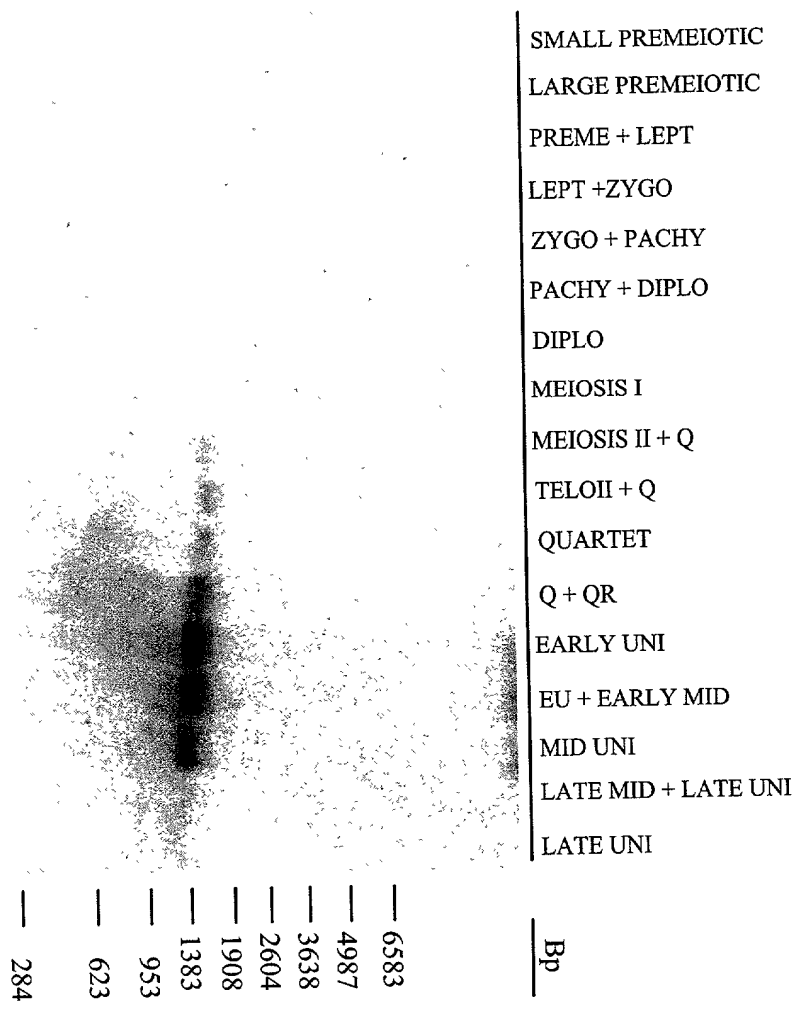
2001 CTGCTAC.....TGTCAGGGCGTCATAGCTCACGGGCTCTCCGGCTAC 2043
      ||||||| ||||||||||||||||||||||||||||||| |||||||
1079 CTGCTACTGTCAGGTGTCAGGGCGTCATAGCTCACGGGCTCTACGGCTAC 1128

2044 ATGAATAAAA...ATGTCACGCTCGTCATTTGCTTTGCCTTTTTTTTTTGG 2090
      ||||||||| | ||||||||||||||||||| |||
1129 ATGAATAAAATGTCACGCTAGCTCGTCATTTGCTTTGCCATTTAAAAAAA 1178

2091 GTTCGTTCTGCGAaCTTCCGTTGCTGTGTGTAATTGTGGCTGCCGGTc 2140
      |
1179 AAAAAAAAAAAAACTCGAG..... 1197

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DEVELOPMENTAL GENE EXPRESSION IN MICROSPORO-  
 GENESIS OF THE MALE FERTILITY GENE BS92-7.  
 23 HR. EXP

FIGURE 7



# Normalized Luciferase Activity as a % of Wildtype

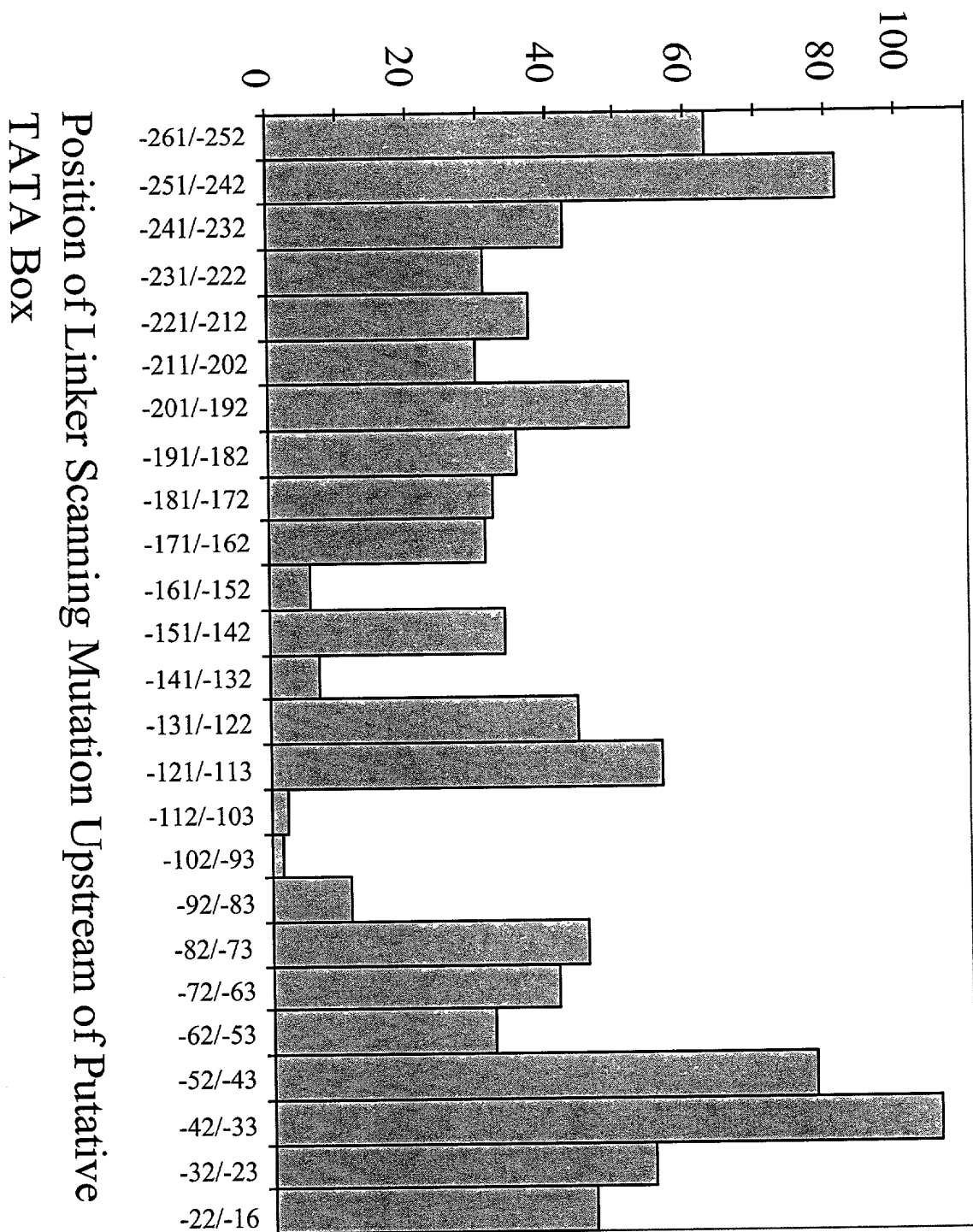


Figure 9

**Figure 10**

1 CGCGTCCTGG ATCGATTGCA AATCTACCTC CAACCAACCC AGCTTTGTAT  
51 CTGCTTACTG TGATCACCAA AGTTGTGCTG ATACGATGTG CGATTATTGC  
101 TCTTTCTTCT CTAGAATGTT CCTGCCGATG CTTTATAAGA GAAGGTTGGT  
151 CAGCATCGAT CTCTGCCAGT GTCTAGCTGA GAACATG

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BS7	MS45	35S	PAT
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BS7:MS45

A632

9  
10  
11  
12  
13



Figure 11



Figure 12

5  
Sorghum V T G A S G F  
GTAACCGGGGCTTCAGGCT 50  
Maize GTAACCGGGGCTTCAGGCT 34  
V T G A S G F  
10  
Sorghum I A S W L I K R L L E S G Y H V  
51 TTATTGCCTCTTGGCTTATCAAACGGCTGCTCGAGTCTGGATATCATGTG 100  
Maize 35 TTGTTGCCTCTTGGCTTATCAAACGGCTCCTCGAGTCTGGATATCATGTG 84  
V A S W L I K R L L E S G Y H V  
20  
Sorghum 101 V G T V R D P G N H Q K T A H L W  
GTAGGGACTGTCAGAGACCCAGGAAATCACCAAAAAACAGCACACCTTTG 150  
Maize 85 GTAGGGACTGTCAGGGACCCAGGAAATCACCAAAAAACAGCCACCTTTG 134  
V G T V R D P G N H Q K T A H L W  
25  
Sorghum 151 K L P G A K E R L Q I V R A D L L  
GAAATTACCTGGTGCCAAAGAGAGGCTGCAAATTGTGCGAGCTGATCTGT 200  
Maize 135 GAAATTACCTGGCGCTAAAGAGAGGCTGCAAATCGTGCGAGCTAATCTGT 184  
K L P G A K E R L Q I V R A N L L  
30  
Sorghum 201 E E G S F D N A V M D C D G V F  
TGGAAGAAGGGAGCTTTGACAATGCTGTGCTGACTGTGATGGCGTCTTC 250  
Maize 185 TGGAAGAAGGGAGCTTCGACAGCGCCGTGATGGCCTGTGAGGGTGTATTC 234  
E E G S F D S A V M A C E G V F  
35  
Sorghum 251 H T A S P V L A K S D S S S K E E  
CACACTGCATCCCCGTGTGCTCGCTAAATCTGATTCTAGTAGCAAGGAGGA 300  
Maize 235 CACACTGCATCCCCGTGCTCGCTAAACCCGACTCTACTAGCAAGGAGGA 284  
H T A S P V L A K P D S T S K E E  
40  
Sorghum 301 T L V P A V N G T L N V L R S C K  
AACGCTTTGTCCAGCAGTAAACGGTACTCTGAATGTGCTAAGATCGTGCA 350  
Maize 285 CACGCTCGTCCCTGCGGTGAACGGTACTCTGAACGTGCTGAGATCGTGCA 334  
T L V P A V N G T L N V L R S C K  
50  
Sorghum 351 K N P F L K R V V L T S S S S A  
AGAAGAACCCATTTCTGAAAAGGGTTGTTCTTACGTCTTCATCATCTGCA 400  
Maize 335 AGAAGAACCCCTTCCTGAAAAGGGTCGTCCTTACGTCTTCGTCGTCTGCG 384  
K N P F L K R V V L T S S S S A

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[illegible]

5	Sorghum	401	GTGAGGATTAGGGATGATGATCAGC.....CTAATATCTCACTGGATGA	444 
10	Maize	385	GTGAGGATCAGGGACGACGGTGGCCAGTCCAGTAACATCTCGCTGGACGA	434 V R I R D D G G Q S S N I S L D E
			T T W S S V P L C E K M Q L W Y A	
	Sorghum	445	AACAACATGGAGCTCTGTGCCACTCTGTGAAAAGATGCAGCTATGGTATG	494 
15	Maize	435	AACGACATGGAGCTCCGTGCCACTCTGCGAAAAGATGCATCTATGGTATG	484 T T W S S V P L C E K M H L W Y A
			L A K V F A E K A A W E F A K E	
20	Sorghum	495	CCCTAGCGAAGGTATTTGCAGAGAAAGCGGCATGGGAATTCGCCAAGGAG	544 
	Maize	485	CCCTAGCCAAGGTATTTGCAGAGAAAGCGGCGTGGGAGTTCGCCAAGGAG	534 L A K V F A E K A A W E F A K E
			N N I D L V T V L P S F V I G P S	
25	Sorghum	545	AACAACATCGACCTTG TGACTGTCCTCCCATCATTTGTGATCGGGCCCAG	594 
	Maize	535	AACGGCATCGACCTTG TGACTGTCCTCCCGTCGTTCTGATCGGGCCCAG	584 N G I D L V T V L P S F V I G P S
30			L S H E L C V T A S D V L G L F Q	
	Sorghum	595	TTTATCCCATGAACTATGTGTTACC GCTTCAGATGTCCTAGGCTTATTCC	644 
	Maize	585	TTTGTCCCACGAGCTATGCGTTACC GCTTCAGACGTCCTAGGCCTATTCC	634 L S H E L C V T A S D V L G L F Q
35			G D T A R F S S Y G R M G Y V H	
	Sorghum	645	AAGGTGACACGGCAAGGTTCA GTTCTTACGGAAGAATGGGATACGTTAC	694 
	Maize	635	AAGGCGACACGGCAAGGTTCA GTCTCGTACGGAAGAATGGGGTACGTCCAC	684 G D T A R F S S Y G R M G Y V H
40			I D D V A T S H I L V	
	Sorghum	695	ATCGACGATGTTGCGACCAGCCACATCCTGGTGT	725
45	Maize	685	ATCGACGACGTTGCGAGCAGCCACATCCTGGTGT	718 I D D V A S S H I L V